SEQUENCE LISTING

(1) GENERAL INFORMATION:	
(A) NAME: sanofi (B) STREET: 32-34 rue Marbeuf (C) CITY: PARIS (E) COUNTRY: FRANCE (F) POSTAL CODE (ZIP): 75008 (G) TELEPHONE: 01 53 77 40 00 (H) TELEFAX: 01 53 77 41 33	
(ii) TITLE OF INVENTION: SR-p70	
(ili) NUMBER OF SEQUENCES: 40	
(iv) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)	
(2) INFORMATION FOR SEQ AD NO: 1:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2874 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(Vi) ORIGINAL SOURCE: (A) ORGANISM: Cebus apella	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1562066	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1	
TGCCTCCCCG CCCGCGCACC CGCCCCGAGG CCTGTGCTCC TCCGAAGGGG ACGCAGCGAA 60	0
GCCGGGGCCC GCGCCAGGCC GGCCGGGACG GACGCCGATG CCCGGAGCTG CGACGGCTGC 120	0
AGAGCGAGCT GCCCTCGGAG GCCGGTGTGA GGAAG ATG GCC CAG TCC ACC ACC Met Ala Gln Ser Thr Thr 1 5	3
ACC TCC CCC GAT GGG GGC ACC ACG TTT GAG CAC CTC TGG AGC TCT CTG Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu His Leu Trp Ser Ser Leu 10 15	l
GAA CCA GAC AGC ACC TAC TTC GAC CTT CCC CAG TCA AGC CGG GAT Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro Gln Ser Ser Arg Gly Asn 25 30 35	9
AAT GAG GTG GGT GGC ACG GAT TCC AGC ATG GAC GTC TTC CAC CTA Asn Glu Val Val Gly Gly Thr Asp Ser Ser Met Asp Val Phe His Leu 40 45 50	,
GAG GGC ATG ACC ACA TCT GTC ATG GCC CAG TTC AAT TTG CTG AGC AGC Glu Gly Met Thr Thr Ser Val Met Ala Gln Phe Asn Leu Leu Ser Ser 55 60 65 70	;
ACC ATG GAC CAG ATG AGC AGC CGC GCT GCC TCG GCC AGC CCG TAC ACC Thr Met Asp Gln Met Ser Ser Arg Ala Ala Ser Ala Ser Pro Tyr Thr 75 80 85	ì

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	AG(Se)	T Se	Th:	r Phe	C GAG e Ası	E ACC	ATG Met	Ser 110	Pro	GCC Ala	CCI Pro	GTC Val	ATO	Pro	TCC Sei	AAC Asn		509	
	Thi	GA0 Asp 120	o Ty	Pro	C GGA C Gly	A CCC	CAC His 125	His	TTC	GAG Glu	GTC Val	ACT Thr 130	Phe	CAC Glr	G CAC	TCC Ser		557	
	Ser 135	Thi	r Ala	a.Ly3	Ser	140	Thr	Trp	Thr	Tyr	Ser 145	Pro	Leu	Leu	Lys	150		605	
	CTC Leu	TAC Tyr	TGC Cys	C CAC	3 A10 1 11e 155	∖ Ala	AAG Lys	ACA Thr	TGC	Pro 160	Ile	CAG Gln	ATC Ile	AAG Lys	GTG Val 165	Ser		65 3	
	GCC Ala	CCA Pro	CCC Pro	Pro 170	Pro	61 y	ACC	GCC Ala	ATC Ile 175	Arg	GCC Ala	ATG Met	CCT Pro	GTC Val 180	Tyr	AAG Lys		701	
	AAG Lys	GCG Ala	GAG G1u 185	ı His	GTG Val	ACC Thr	GA& Asp	ATC Ile 90	GTG Val	AAG Lys	CGC	TGC -Cys	CCC Pro 195	Asn	CAC His	GAG Glu	. *	749	
	CTC	GGG Gly 200	Arg	GAC Asp	TTC Phe	AAC Asn	GAA Glu 205	GGA Gly	CAG Gln	TCT	GCC Ala	CCA Pro 210	GCC Ala	AGC Ser	CAC His	CTC Leu		797	
	ATC Ile 215	CGT Arg	GTG Val	GAA Glu	GGC Gly	AAT Asn 220	AAT Asn	CTC Leu	TCG Ser	CAG	TAT Tyr 225	GTG Val	GAC Asp	GAC Asp	CCT Pro	GTC Val 230		845	
	Thr	Gly	Arg	Gln	Ser 235	Val	GTG Val	Val	Pro	Tyr 240	&1u	Pro	Pro	Gln	Val 245	Gly		893	
	Thr	Glu	Phe	Thr 250	Thr	Ile	CTG Leu	Tyr	Asn 255	Phe	Met	gha	Asn	Ser 260	Ser	Суз		941	
/	GTG Val	GGG Gly	GGC Gly 265	ATG Met	AAC Asn	CGA Arg	CGG Arg	CCC Pro 270	ATC Ile	CTC Leu	ATC Ile	ATC Ile	ITC ILe 279	ACC Thr	CTG Leu	GAG Glu		989	
	ACG Thr	CGG Arg 280	GAT Asp	GGG Gly	CAG Gln	GTG Val	CTG Leu 285	GGC Gly	CGC Arg	CGG Arg	TCC Ser	TTC Phe 290	GAG Glu	G1 X	CGC	ATC Ile		1037	
	TGC Cys 295	GCC Ala	TGT Cys	CCT	GGC Gly	CGC Arg 300	GAC Asp	CGA Arg	AAA Lys	GCC Ala	GAT Asp 305	GAG Glu	GAC Asp	CAC His	TAC	370 yra cee		1085	
	GAG Glu	CAG Gln	CAG Gln	GCC Ala	TTG Leu 315	TAA Asn	GAG Glu	AGC Ser	TCC Ser	GCC Ala 320	AAG Lys	AAC Asn	GGG Gly	GCT Ala	GCC Ala 325	Ser		1133	
	AAG Lys	CGC Arg	GCC Ala	TTC Phe 330	AAG Lys	CAG Gln	AGT Ser	CCC Pro	Pro 335	GCC Ala	GTC Val	CCC Pro	GCC Ala	CTG Leu 340	GGC Gly	CCG Pro	\	181	
	JI Y	val	345	гуз	Arg	Arg	CAC His	350	Asp	Glu	Asp	Thr	Tyr 355	Tyr	Leu	Gln		1229	\
1	GTG Val	CGA Arg 360	GGC Gly	CGC Arg	GAG Glu	AAC Asn	TTC Phe 365	GAG . Glu	ATC Ile	CTG Leu	ATG Met	AAG Lys 370	CTG Leu	AAG Lys	GAG Glu	AGC Ser	:	1277	

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	CT0 Let 375	1 GI	G CTO	J ATO	G GA	380	ı Val	CCC Pro	G CAG	CCG Pro	CTC Leu 385	ı Val	A GAC . Asp	Ser	TAT	CGG Arg 390		13.25
	CAC Gl:	G CAC n Glr	CAC 1 Glr	G CAC	G CTC 1 Let 395	ı Leu	CAG Gln	AGG Arg	CCG Pro	AGT Ser 400	His	CTA Leu	CAG Gln	CCC Pro	CCA Pro 405	TCC Ser		1373
	TAC Tyr	: GG(G CCC	Val 418	. Lei	TCG Ser	Pro	ATG Met	AAC Asn 415	Lys	GTG Val	CAC His	GGG Gly	GGC Gly 420	GTG Val	AAC Asn		1421
	AAG Lys	CTC Leu	9 CCC 1 Pro 425	Sez	Val	AAC Asn	CAG Gln	CTG Leu 430	Val	G1 Y	CAG Gln	CCT Pro	CCC Pro 435	CCG Pro	CAC His	AGC Ser		1469
	TCG	GCA Ala 440	Ala	AÇA Thr	CCC Pro	AAC	CTG Leu 445	GGA Gly	CCT	GTG Val	GGC Gly	TCT Ser 450	Gly	ATG Met	CTC Leu	AAC Asn		1517
	AAC Asn 455	His	GGC	CAC His	GCA Ala	GTG Val 460	PAO	GCC Ala	AAC Asn	AGC Ser	GAG Glu 465	ATG Met	ACC Thr	AGC Ser	AGC Ser	CAC His 470		1565
	GGC Gly	ACC Thr	CAG Gln	TCC	ATG Met 475	GTC Val	TCG Ser	GIY GIY	TCC Ser	CAC His 480	TGC Cys	ACT Thr	CCG Pro	CCA Pro	CCC Pro 485	CCC		1613
	TAC Tyr	CAC His	GCC	GAC Asp 490	Pro	AGC Ser	CTC	GTC Val	AGT Set 495	TTT Phe	TTA Leu	ACA Thr	GGA Gly	TTG Leu 500	GGG Gly	TGT Cys		1661
	CCA Pro	AAC Asn	TGC Cys 505	ATC Ile	GAG Glu	TAT Tyr	TTC Phe	ACG Thr 510	TCC Ser	cye cye	GGG Gly	Leu	CAG Gln 515	AGC Ser	ATT Ile	TAC Tyr		1709
	CAC His	CTG Leu 520	CAG Gln	AAC Asn	CTG Leu	ACC Thr	ATC Ile 525	GAG Glu	GAC Asp	CTG Leu	GI W	GCC Ala §30	CTG Leu	AAG Lys	ATC Ile	CCC		1757
/	GAG Glu 535	CAG Gln	TAT Tyr	CGC Arg	ATG Met	ACC Thr 540	ATC	TGG Trp	CGG Arg	GGC Gly	CTG Leu 545	CAG. Gln	GAC Asp	CTG Leu	AAG Lys	CAG Gln 550		1805
	GGC Gly	CAC His	GAC Asp	TAC Tyr	GGC Gly 555	GCC Ala	GCC Ala	GCG Ala	CAG Gln	CAG Gln 560	CTG Leu	CTC Leu	CGG	TCC Ser	AGC Ser 565	AAC Asn		1853
		GCC Ala		ATT Ile 570	TCC Ser	ATC Ile	GGC GGC	GGC Gly	TCC Ser 575	GGG Gly	GAG Glu	CTG Leu	ÇAG Gln	CGC Arg 580	CAG	CGG Arg		1901
	GTC Val	ATG Met	GAG Glu 585	GCC Ala	GTG Val	CAC His	TTC Phe	CGC Arg 590	GTG Val	CGC Arg	CAC His	ACC Thr	ATC Ile 595	ACC Thr	ATC Ile	CCC CCC		1949
	AAC Asn	CGC Arg 600	GGC Gly	GGC Gly	CCC Pro	GGC Gly	GCC Ala 605	GGC Gly	CCC Pro	GAC Asp	GAG Glu	TGG Trp 610	GCG Ala	GAC . Asp	TTC Phe	GGC Gly	\	1997
	TTC Phe 615	GAC Asp	CTG Leu	CCC Pro	GAC Asp	TGC Cys 620	AAG Lys	GCC Ala	CGC Arg	Lys	CAG Gln 625	CCC Pro	ATC . Ile	AAG Lys	GAG Glu	GAG Glu 630		2045
	TTC Phe	ACG Thr	GAG Glu	GCC Ala	GAG Glu 635	ATC Ile	CAC His	TGAG	GGGC	CG G	GCCC.	AGCC.	A GA	ĢCCT	GTGC			2006
	CACC	GCCC	AG A	GACC	CAGG	c cc	CCTC	GCTC	TCC	TTCC:	TGT (GTCC	AAAA	ct G	CCTC	CGGAG	;	2156
																CCTCA		2216
														_				

GAGAGGCCCA	GCCACCAAAG	CCGCCTGCGG	ACAGCCTGAG	TCACCTGCAG	227
AGCTGCCCTA	ATGCTGGGCT	TGCGGGGCAG	GGGCCGGCCC	ACTCTCAGCC	233
CGGGCGTGCT	CCATGGCAGG	CGTGGGTGGG	GACCGCAGTG	TCAGCTCCGA	239
TCATCCTAGA	GACTCTGTCA	TCTGCCGATC	AAGCAAGGTC	CTTCCAGAGG	2456
CTTCGCTGGT	GGACTGCCAA	AAAGTATTTT	GCGACATCTT	TTGGTTCTGG	2516
GCAGCCAAGC	GACTGTGTCT	GAAACACCGT	GCATTTTCAG	GGAATGTCCC	2576
GGGACTCTCT	CTGCTGGACT	TGGGAGTGGC	CTTTGCCCCC	AGCACACTGT	2636
ACCGCCTCCT	TCCTGCCCCT	AACAACCACC	AAAGTGTTGC	TGAAATTGGA	2696
GAAGGCGCAA	CCCCTCCCAG	GTGCGGGAAG	CATCTGGTAC	CGCCTCGGCC	2756
AGCCTGGCCA	CAGTCACCTC	TCCTTGGGGA	ACCCTGGGCA	GAAAGGGACA	2316
AGAGGACCGG	AAATTGTCAA	TATTTGATAA	AATGATACCC	TTTTCTAC	2874
	AGCTGCCCTA CGGGCGTGCT TCATCCTAGA CTTCGCTGGT GCAGCCAAGC GGGACTCTCT ACCGCCTCCT GAAGGCGCAA AGCCTGGCCA	AGCTGCCCTA ATGCTGGGCT CGGGCGTGCT CCATGGCAGG TCATCCTAGA GACTCTGTCA CTTCGCTGGT GGACTGCCAA GCAGCCAAGC GACTGTGTCT GGGACTCTCT CTGCTGGACT ACCGCCTCCT TCCTGCCCCT GAAGGCGCAA CCCCTCCCAG AGCCTGGCCA CAGTCACCTC	AGCTGCCCTA ATGCTGGGCT TGCGGGGCAG CGGGCGTGCT CCATGGCAGG CGTGGGTGGG TCATCCTAGA GACTCTGTCA TCTGCCGATC CTTCGCTGGT GGACTGCCAA AAAGTATTTT GCAGCCAAGC GACTGTGTCT GAAACACCGT GGGACTCTCT CTGCTGGACT TGGGAGTGGC ACCGCCTCCT TCCTGCCCCT AACAACCACC GAACGCGCAA CCCCTCCCAG GTGCGGGAAG AGCCTGGCCA CAGTCACCTC TCCTTGGGGA	AGCTGCCCTA ATGCTGGGCT TGCGGGGCAG GGGCCGGCCC CGGGCGTGCT CCATGGCAGG CGTGGGTGGG GACCGCAGTG TCATCCTAGA GACTCTGTCA TCTGCCGATC AAGCAAGGTC CTTCGCTGGT GGACTGCCAA AAAGTATTTT GCGACATCTT GCAGCCAAGC GACTGTGTCT GAAACACCGT GCATTTTCAG GGGACTCTCT CTGCTGGACT TGGGAGTGGC CTTTGCCCCC ACCGCCTCCT TCCTGCCCCT AACAACCACC AAAGTGTTGC GAACGCGCAA CCCCTCCCAG GTGCGGGAAG CATCTGGTAC AGCCTGGCCA CAGTCACCTC TCCTTGGGGA ACCCTGGGCA	AGCTGCCCTA ATGCTGGGCT TGCGGGGGCAG GGGCCGGCCC ACTCTCAGCC CGGGCGTGCT CCATGGCAGG CGTGGGTGGG GACCGCAGTG TCAGCTCCGA TCATCCTAGA GACTCTGTCA TCTGCCGATC AAGCAAGGTC CTTCCAGAGG CTTCGCTGGT GGACTGCCAA AAAGTATTTT GCGACATCTT TTGGTTCTGG GCAGCCAAGC GACTGTGTCT GAAACACCGT GCATTTTCAG GGAATGTCCC GGGACTCTCT CTGCTGGACT TGGGAGTGGC CTTTGCCCCC AGCACACTGT ACCGCCTCCT TCCTGCCCCT AACAACCACC AAAGTGTTGC TGAAATTGGA GAACGCGCAA CCCCTCCCAG GTGCGGAAG CATCTGGTAC CGCCTCGGCC AGCCTGGCCA CAGTCACCTC TCCTTGGGGA ACCCTGGGCA GAAAGGGACA AGAGGACCGG AAATTGTCAA TATTTGATAA AATGATACCC TTTTCTAC

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 637 amino acids
 - (B) TYPE: amind acid
 (D) TOPOLOGY: linear
- (5) ISISBOSI: III(ear

(ii) MOLECULE TYPE: protein

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Gln Ser Thr Thr Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
1 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser 35

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
50 55

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Aro Thr His 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala 100 105 110

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu 115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr 130 135 140

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro 145 150 155

Ile Gln Ile Lys Val Ser Ala Pro Pro Pro Pro Gly Thr Ala Ile Arg 165 170 175

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys
180 185 190

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln S r

Mb

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Pro Tyr Glu Pao Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys Asq Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg 275 280 285 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala
290 295 300 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala 305 310 315 320 Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala 325 Val Pro Ala Leu Gly Pro Gly Val Lys Lys Arg Arg His Gly Asp Glu 340 Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu 355 Met Lys Leu Lys Glu Ser Leu Glu Leu Wet Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser 395 400 His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly
420 425 430 Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Ser Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Ser Glu Met Thr Ser Ser His Gly Thr Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe 485 490 495 Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln 500 505 510 Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Gly Ala Ala Ala Gln Gln 545 550 555 560 Leu Leu Arg Ser Ser Asn Ala Ala Ile Ser Ile Gly Gly Ser Gly 565 570 575 Glu Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg

His Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Ala Gly Pro Asp

580

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Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln Gln Ser

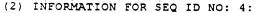
AGC ACG GCC AAG TCA GCC ACC TGG ACG TAC TCC CCA CTC TTG AAG AAA

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S 1	er .35	Thi	r Al	a Ly	s Se	r Ala 140	a Thi	Tr) Thi	с Ту	r Ser 145) Le	ı Let	ı Ly	s Lys 150		٠
ī.	TC.	TAC Ty:	TG: Cy	c cad s Gli	G ATO	e Ala	AAC a Lys	ACI Thi	A TGO	CCC Pro 160) Ile	CAC Glr	ATO	C·AA0 ∋ Lys	G GT G Va 16	G TCC l Ser		653
G A	CC Na	200	A CC	G CC0 0 Pro 170	o Pro	G GG(ACC Thr	GCC Ala	175	Arc	G GCC J Ala	ATC Met	CC1	Val	Ty.	I AAG Lys	:	701
A L	AG ys	GC à	GA0	a His	GTC Val	G ACC	GAC Asp	11e	. Val	AAC Lys	CGC	TGC Cys	CCC Pro	Asn	CAC His	GAG Glu		749
L L	TC eu	GGG Gly 200	Arc	SAC SEA	Phe	AAC Asr	GAA Glu 205	. Gly	CAG Gln	TCT Ser	GCC	CCA Pro 210	Ala	AGC	CAC	CTC Leu		797
I	TC le 15	CGT	GTC Val	G GAA	G G G G G G G G G G G G G G G G G G G	AAT Asn 220	Asn	CTC Leu	TCG	CAG Gln	TAT Tyr 225	Val	GAC Asp	GAC Asp	CC1	GTC Val 230		845
A)	CC hr	GGC Gly	AGC Arç	G CAG	AGC Ser 235	· Val	GTG Val	GTG Val	Pro	TAT Tyr 240	Glu	CCA Pro	CCA Pro	CAG Gln	GTC Val 245	GGG Gly		893
A)	CA nr	GAA Glu	TTC Phe	ACC Thr 250	Thr	ATC Ile	CTG Leu	TAC	AAC Asn 255	TTC Phe	ATG Met	TGT Cys	AAC Asn	AGC Ser 260	AGC	TGT Cys	,	941
G? Vá	rG al	GGG Gly	GGC G1 y 2 6 5	Met	AAC Asn	CGA Arg	CGG Arg	CCC Pro 270	ATC Ile	CTC Leu	ATC Ile	ATC Ile	ATC Ile 275	Thr	CTG Leu	GAG Glu		989
AC Th	ır	CGG Arg 280	GAT Asp	GGG Gly	CAG Gln	GTG Val	CTG Leu 285	GGC Gly	CGC Arg	COC ALG	TCC	TTC Phe 290	GAG Glu	GLY	CGC	ATC Ile	•	1037
T C Y 2 S	/S	GCC Ala	TGT Cys	CCT Pro	GGC	CGC Arg 300	GAC Asp	CGA Arg	AAA Lys	GCC Ala	GAT Asp 305	GAG Glu	GAC Asp	CAC His	TAC Tyr	CGG Arg		1085
GA G1	iG .u	CAG Gln	CAG Gln	GCC Ala	TTG Leu 315	AAT Asn	GAG Glu	AGC Ser	TCC Ser	GCC Ala 320	AAG Lys	AAC Asn	ezh Æœ	GCT Ala	GCC Ala 325	AGC Ser		1133
AA Ly	G (CGC Arg	GCC Ala	TTC Phe 330	Lys	CAG Gln	AGT Ser	CCC Pro	CCT Pro 335	GCC Ala	GTC Val	CCC Pro	GCC Ala	CTG Leu 340	GGC Gly	CCG Pro	*	1181
GG G1	T (GTG Val	AAG Lys 345	AAG Lys	CGG Arg	CGG Arg	CAC His	GGA Gly 350	GAC Asp	GAG Glu	GAC Asp	ACG Thr	TAC Tyr 355	TAC Tyr	CrG	CAG Gln		1229
GT Va	1	CGA Arg 360	GGC Gly	CGC Arg	GAG Glu	AAC Asn	TTC Phe 365	GAG Glu	ATC Ile	CTG Leu	ATG Met	AAG Lys 370	CTG Leu	AAG Lys	GAG Glu	AGC Ser	\	1277
CT Le	u	GAG Glu	CTG Leu	ATG Met	GAG Glu	TTG Leu 380	GTG Val	CCG Pro	C AG Gln	CCG Pro	CTG Leu 385	GTA Val	GAC Asp	TCC Ser	TAT Tyr	CGG Arg 390		1325
CA Gl:	G C	AG Fln	CAG Gln	CAG Gln	CTC Leu 395	CTA Leu	CAG Gln	AGG Arg	CCG Pro	AGT Ser 400	CAC His	CTA Leu	CAG Gln	CCC Pro	CCA Pro 405	TCC Ser		373
TAC Ty:	ro	GG Gly	CCG Pro	GTC Val 410	CTC Leu	TCG Ser	CCC Pro	ATG Met	AAC Asn 415	AAG Lys	GTG Val	CAC His	GGG Gly	GGC Gly 420	GTG Val	AAC Asn		1421
AA	3 0	TG	ccc	тсс	GTC	AAC	CAG	CTG	GTG	GGC	CAG	CCT	ccc	CCG	CAC	AGC		1469

Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser	
TCG GCA GCT ACA CCC AAC CTG GGA CCT GTG GGC TCT GGG ATG CTC AAC Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Ser Gly Met Leu Asn 440 450	1517
AAC CAC GGC CAC GCA GTG CCA GCC AAC AGC GAG ATG ACC AGC AGC CAC Asn His Gly Nis Ala Val Pro Ala Asn Ser Glu Met Thr Ser Ser His 455	1565
GGC ACC CAG TCC ATG GTC TCG GGG TCC CAC TGC ACT CCG CCA CCC CCG Gly Thr Gln Ser Net Val Ser Gly Ser His Cys Thr Pro Pro Pro 435 480 485	1613
TAC CAC GCC GAC CCC AGC CTC GTC AGG ACC TGG GGG CCC TGAAGATCCC Tyr His Ala Asp Pro Ser Leu Val Arg Thr Trp Gly Pro 490 495	1662
CGAGCAGTAT CGCATGACCA TCTGGCGGGG CCTGCAGGAC CTGAAGCAGG GCCACGACTA	Á 1722
CGGCGCCGCC GCGCAGCAGC TGCTGCGCTC CAGCAACGCG GCCGCCATTT CCATCGGCG	3 1782
CICCGGGGAG CIGCAGCGCC AGCGGGTCAT GGAGGCCGTG CACTICCGCG TGCGCCACAG	1842
CATCACCATC CCCAACCGCG GCGGCCCCGG CGCCGGCCCC GACGAGTGGG CGGACTTCGG	3 1902
CTTCGACCTG CCCGACTGCA AGGCCCGCAA CCAGCCCATC AAGGAGGAGT TCACGGAGG	1962
CGAGATCCAC TGAGGGGCCG GGCCCAGCCA GAGCCTGTGC CACCGCCCAG AGACCCAGGC	2022
CGCCTCGCTC TC	2034



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Gln Ser Thr Thr Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
1 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser 35

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala din 50 60

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala 65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His 85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu 115

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr 130 135 140



Ser Pro Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val Ser Ala Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys
180 185 190 Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Pro Tyr 225 230 235 Glu Pro Pro Gln val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu 260 265 270 Ile Ile Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg 275 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala 290 300 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala 305 310 315 320 Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu Gly Pro Gly Val Lys Lys Arg Arg His Gly Asp Glu 340 345 Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glo Asn Phe Glu Ile Leu 355 360 365 Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro 370 380 Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser 385 395 400 His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly 420 425 Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Ser Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Ser Glu Met Thr Ser Ser His Gly Thr Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr Trp Gly Pro

- (2) INFORMATION FOR SEQ ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2156 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(A) ORGANISM: Homo sapiens

(11) MOLECULE TYPE: cDNA
(V1) ORIGINAL SOURCE:

FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 33..1940 (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 5: GCGAGCTGCC CTCGGAGGCC GGCGTGGGGA AG ATG GCC CAG TCC ACC GCC ACC 53 Met Ala Gln Ser Thr Ala Thr TCC CCT GAT GGG GGC ACC ACG TTT GAG CAC CTC TGG AGC TCT CTG GAA Ser Pro Asp Gly Gly Thr Thr Phe Glu His Leu Trp Ser Ser Leu Glu 101 15 CCA GAC AGC ACC TAC TTC GAC CTT CCC CAG TCA AGC CGG GGG AAT AAT 149 Pro Asp Ser Thr Tyr Phe Asp Leu Pro Gln Ser Ser Arg Gly Asn Asn GAG GTG GTG GGC GGA ACG GAT TCC AGC ATG GAC GTC TTC CAC CTG GAG Glu Val Val Gly Gly Thr Asp er Ser Met Asp Val Phe His Leu Glu 197 GGC ATG ACT ACA TCT GTC ATG GCC CAG TTC AAT CTG CTG AGC AGC ACC Gly Met Thr Thr Ser Val Met Ala Oln Phe Asn Leu Leu Ser Ser Thr 245 ATG GAC CAG ATG AGC AGC CGC GCG GCC TCG GCC AGC CCC TAC ACC CCA Met Asp Gln Met Ser Ser Arg Ala Ala Ser Ala Ser Pro Tyr Thr Pro 293 80 GAG CAC GCC GCC AGC GTG CCC ACC CAC TCG OCC TAC GCA CAA CCC AGC 341 Glu His Ala Ala Ser Val Pro Thr His Ser Pro Tyr Ala Gln Pro Ser TCC ACC TTC GAC ACC ATG TCG CCG GCG CCT GTC ATC CCC TCC AAC ACC 389 Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn Thr 110 GAC TAC CCC GGA CCC CAC CAC TTT GAG GTC ACT TTC CAG CAG TCC AGC 437 Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln Gln Ser Ser ACG GCC AAG TCA GCC ACC TGG ACG TAC TCC CCG CTC TTG AAG AAA CTC 485 Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Leu Lys Lys Leu TAC TGC CAG ATC GCC AAG ACA TGC CCC ATC CAG ATC AAG GTG TCC ACC 533 Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val Ser The CCG CCA CCC CCA GGC ACT GCC ATC CGG GCC ATG CCT GTT TAC AAG AAA 581 Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys 175 GCG GAG CAC GTG ACC GAC GTG GTG AAA CGC TGC CCC AAC CAC GAG CTC Ala Glu His Val Thr Asp Val Val Lys Arg Cys Pro Asn His Glu Leu GGG AGG GAC TTC AAC GAA GGA CAG TCT GCT CCA GCC AGC CAC CTC ATC Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro Ala Ser His L u Ile 677 205

	Arc	GT G Va	G GA 1 G1	A GG u Gl	C AA y As 22	n As	I CTO	I Se	G CA r Gl	G TA' n Ty: 22:	r Val	G GA l As	T GA p As	C CC P Pr	T GT 0 Va 23	C ACC 1 Thr 0	725	١
	GGC Gly	AG Ar	G CA g Gl	G AG n Se . 23	r Va	C GTO	G GTO	G CCC	TA' 5 Ty: 24	r Glu	G CCA	A CC	A CAG	G GT n Va 24:	1 G1	G ACG y Thr	773	
	GAA Glu	TT:	C AC e Th	ξ In	C AT	C CTO	TAC 1 Tyr	AA0 Asr 255	ı Phe	C ATO	G TGT	AA ? IEA 8	2 AGC	r Se	C TG	T GTA s Val	821	
	GGG Gly	GG(G1: 26:	y Me	G AA t As	C CG	G CGC g Arc	F CCC F Pro 270) Ile	CTC	ATO	ATC Ile	ATC 116 275	Th:	CTC Let	G GAO	G ATG 1 Met	869	
4	CGG Arg 280	AS	r GGG	G CA y Gli	G GT n Val	CTC L Xeu 285	GGC Glý	CGC	CGC Arg	TCC Ser	Phe 290	Gli	GGC Gly	CGC Arc	J Ile	TGC Cys 295	9.17	
į	GCC Ala	TGT	CC:	r GG(o Gl)	CGG Y Arg 300	, Asp	ALGA	AAA Lys	GCT Ala	GAT Asp 305	Glu	GAC Asp	CAC His	TAC	CGC Arc 310	GAG Glu	965	
Ć	CAG Gln	CAC Glr	GC0 Ala	CTC Let 315	ı Asr	GAG Glu	AGC Ser	TCC Sei	GCC Ala 320	Lys	AAC Asn	GGG Gly	GCC Ala	GCC Ala 325	Ser	AAG Lys	1013	
,	GT Arg	GCC Ala	TTC Phe 330	Lys	G CAG	AGC Ser	CCC Pro	CCT Pro 335	Ala	GTC Val	CCC Pro	GCC Ala	CTT Leu 340	Gly	GCC Ala	GGT	1061	
V	TG al	AAG Lys 345	гλа	G CGG	cgg Arg	CAT	GGA Gly 350	GAC Asp	GAG Glu	GAQ Asp	ACG Thr	TAC Tyr 355	TAC Tyr	CTT Leu	CAG Gln	GTG Val	1109	
-	GA FG 60	GGC Gly	CGG Arg	GAG Glu	AAC Asn	TTT Phe 365	GAG Glu	ATC Ile	CTG Leu	ATG Met	AAG Lys 370	CTG	AAA Lys	GAG Glu	AGC Ser	CTG Leu 375	1157	
∕'G G	AG lu	CTG Leu	ATG Met	GAG Glu	TTG Leu 380	GTG Val	CCG Pro	CAG Gln	CCA Pro	CTG Leu 385	GTG Val	GAC Asp	Ser	TAT Tyr	CGG Arg 390	CAG Gln	1205	
G	AG ln	CAG Gln	CAG Gln	CTC Leu 395	CTA Leu	CAG Gln	AGG Arg	CCG Pro	AGT Ser 400	CAC His	CTA Leu	CAG Gln	CCC Pro	Pro 405	TCC Ser	TAC Tyr	1253	
G	GG ly	CCG Pro	GTC Val 410	CTC Leu	TCG Ser	CCC Pro	ATG Met	AAC Asn 415	AAG Lys	GTG Val	CAC His	GGG Gly	GGC Gly 420	ATG Met	2AA neA	AAG Lys	1301	
L.	eu	CCC Pro 425	TCC	GTC Val	AAC Asn	CAG Gln	CTG Leu 430	GTG Val	GGC Gly	CAG Gln	CCT Pro	CCC Pro 435	CCG Pro	CAC His	AGT Ser	TCG	1349	
^-	CA d la 2 40	GCT Ala	ACA Thr	CCC Pro	AAC Asn	CTG Leu 445	GGG Gly	CCC Pro	GTG Val	GGC Gly	CCC Pro 450	GGG Gly	ATG Met	CTC Leu	AAC Asn	AAC Asn 455	1397	
C.A Hi	AT (GGC Gly	CAC His	GCA Ala	GTG Val 460	CCA Pro	GCC Ala	AAC Asn	GGC Gly	GAG Glu 465	ATG Met	AGC Ser	AGC Ser	AGC Ser	CAC His 470	AGC Ser	1445	\
GC Al	a c	CAG Gln	TCC Ser	ATG Met 475	GTC Val	TCG Ser	GGG Gly	Ser	CAC His 480	TGC Cys.	ACT Thr	CCG Pro	CCA Pro	CCC Pro 485	CCC Pro	TAC Tyr	1493	
CA Hi	S A	120	GAC Asp 490	CCC Pro	AGC Ser	CTC Leu	val:	AGT Ser 495	TTT Phe	TTA . Leu	ACA (Gly	TTG Leu 500	GGG Gly	TGT Cys	CCA Pro	1541	

AAC Asn	TGC Cys 505	IIe	GAG Glu	TAT Tyr	TTC Phe	ACC Thr 510	TCC Ser	CAA Gln	GGG Gly	TTA Leu	CAG Gln 515	AGC Ser	ATT	TAC Tyr	CAC His		1589
CTG Leu 520	373G 318	AAC Asn	CTG Leu	ACC Thr	ATT Ile 525	GAG Glu	GAC Asp	CTG Leu	GGG Gly	GCC Ala 530	CTG Leu	AAG Lys	ATC Ile	CCC Pro	GAG Glú 535		1637
CAG Gln	TAC	CGC	ATG Met	ACC Thr 540	ATC Ile	TGG Trp	CGG Arg	GGC Gly	CTG Leu 545	Gln	GAC Asp	CTG Leu	AAG Lys	CAG Gln 550	GGC Gly		1685
CAC Hís	GAC Asp	TAC Tyr	AGC Ser 555	ACC	GCG Ala	CAG Gln	CAG Gln	CTG Leu 560	CTC Leu	CGC Arg	TCT Ser	AGC Ser	AAC Asn 565	GCG Ala	GCC Ala		1733
ACC Thr	ATC Ile	TCC Ser 570	ATC Ile	GGC Gly	ejh gec	TCA Ser	GGG Gly 575	GAA Glu	CTG Leu	CAG Gln	CGC Arg	CAG Gln 580	CGG Arg	GTC Val	ATG Met		1781
GAG Glu	GCC Ala 585	GTG Val	CAC His	TTC Phe	CGC Arg	OTG Val 590	CGC Arg	CAC His	ACC Thr	ATC Ile	ACC Thr 595	ATC	CCC Pro	AAC Asn	CGC Arg		1829
GGC Gly 600	GGC Gly	CCA Pro	GGC Gly	GJ Y GGC	GGC Gly 605	CCT Pro	AAC Asp	GAG Glu	TGG Trp	GCG Ala 610	GAC Asp	TTC Phe	GGC Gly	TTC Phe	GAC Asp 615		1877
CTG Leu	CCC Pro	GAC Asp	TGC Cys	AAG Lys 620	GCC Ala	CGC Arg	AAG Lys	dac Glin	CCC Pro 625	ATC Ile	AAG Lys	GAG Glu	GAG Glu	TTC Phe 630	ACG Thr	,	1925
GAG Glu	GCC Ala	GAG Glu	ATC Ile 635	CAC His	TGAG	GGCC	TC G	CCTG	gC10	C AG	CCTG	ccc	ACC	GCCC	AGA		1980
GACC	CAAG	CT G	CCTC	CCCT	C TC	CTTC	CTGT	GTG	TCCA	AAA	CTGC	CTCA	.GG A	.GGCA	GGACC	:	2040
TTCG	GGCT	GT G	ccc	GGGA	A AG	GCAA	GGTC	CGG	CCCA	rcd/	CCAG	GCAC	CT C	ACAG	GCCCC	:	2100
AGGA.	AAGG	cc c	AGCC.	ACCG.	A AG	CCGC	CTGT	GGA	CAGC	CTG .	AGTC	ACCT	GC A	.GAAC	C		2156

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 636 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu 1 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro 20 25 30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser 35 40 45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln 50

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala 65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His 85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Dys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Ala Met Pro Val Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser 195 200 Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln 210 220 Tyr Val Asp Asp Pro Val Tha Gly Arg Gln Ser Val Val Pro Tyr 230 Glu Pro Pro Gln Val Gly Thr Gly Phe Thr Thr Ile Leu Tyr Asn Phe 250 Met Cys Asn Ser Ser Cys Val Gly Gy Met Asn Arg Arg Pro Ile Leu 260 265 270 Ile Ile Ile Thr Leu Glu Met Arg Asp Cly Gln Val Leu Gly Arg Arg 275 280 285 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala 290 295 300 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gla Ser Pro Pro Ala 325 330 Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg Has Gly Asp Glu 340 345 Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu 355 Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro cln Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro 385 390 395 His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln 505 Gly Lev Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Deu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Gly Ala Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg Ser Set Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His 580 590 Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His 630 (2) INFORMATION FOR SEQ ID NO:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 2040 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (Vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mus musculus
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 124..1890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGATCTCCCT GTGGCCTGCA GGGGACTGAG CCAGGGAGTA GATGCCCTGA GACCCCAAGG 60 GACACCCAAG GAAACCTTGC TGGCTTTGAG AAAGGGATCG TCTCTCTCT GCCCAAGAGA 120 AGC ATG TGT ATG GGC CCT GTG TAT GAA TCC TTG GGG CAG GCC CAG TTG 168 Met Cys Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe AAT TTG CTC AGC AGT GCC ATG GAC CAG ATG GGC AGC CGT GCG GCC CCG 216 Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro GCG AGC CCC TAC ACC CCG GAG CAC GCC GCC AGC GCG CCC ACC CAC TCG 264 Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser CCC TAC GCG CAG CCC AGC TCC ACC TTC GAC ACC ATG TCT CCG GCG CCT Pro Tyr Ala Gln Pro Ser Ser Thr Ph Asp Thr M t Ser Pro Ala Pro 312 50

GTC ATC CCT TCC AAT ACC GAC TAC CCC GGC CCC CAC CAC TTC GAG GTC

	Va	1 11	.e 1	Pro	Sei	r Ası	n Th	r As ₁	p Ty	r Pr	o G1	y Pr	0 Hi 7	s Hi S	s Ph	e Gl	u Val	•	
	3	9/2n	e (∍1n	Glr	1 Se:	r Se. 8!	r Th	r Al	a Ly	s Se.	r Ala 9	a Thi	r Tr	p Th	r Ty	C TCC r Ser 95	•	408
		o Le	7	Leu \	Lys	100	s Let	и Туі	c Cy:	s Gl	n Ile 105	e Ala	a Lys	s Th.	r Cy:	s Pr	C ATC o Ile O		456
	GA:	G AT n Il	e I	KAJ .ys	GTG Val 15	. Sei	C ACA	A CCA	A CCI	Pro 120	o Pro	GGG Gly	ACC Thi	G GCC	2 ATC a Ile 125	e Ar	G GCC g Ala		504
	AT(G CC t Pr	0 V	TC al 30	TAC Tyr	AAC	AAC Lys	G GCA B Ala	GA0 Glu 135	His	r GTC 5 Val	ACC Thr	GAC Asp	ATT 116	e Val	L Lys	G CGC B Arg		552
	TG0 .Cys	CCG Pro 14:	O A	AC .sn	CAC His	GAG Glu	CTI	GGA Gly 150	Arg	GAC Asp	TTC Phe	TAA : ne,	GAA Glu 155	ı Gly	A CAC	TC1	GCC Ala		600
	Pro	A A L	T A	GC er	CAC His	CTC	Ile 165	: A/Ęg	GTA Val	GAA Glu	A GGC 1 Gly	AAC Asn 170	Asn	CTC Leu	GCC Ala	CAC Glr	TAC Tyr 175		648
	GTC Val	GA:	C G.	AC sp	CCT Pro	GTC Val 180	Thr	GGA Gly	AGG	CAG Glm	AGT Ser 185	Val	GTT Val	GTG Val	CCG Pro	TAT Tyr 190	GAA Glu		6 96
	PLO	PIC	ص	Ln	195	GTÅ	Thr	Glu	Phe	200	Thr	Ile	Leu	Tyr	205	Phe	ATG Met		744
	TGT Cys	AAC Asn		GC . er :	AGC Ser	TGT Cys	GTG Val	GGG	GGC Gly 215	ATG Met	TAA neA	CGG Arg	AGG Arg	CCC Pro 220	Ile	CTT Leu	GTC Val		792
/	ııe	225	Tr	ır .	Leu	Glu	Thr	Arg 230	Asp	Gly	CAG Gln	Val	Leu 235	Gly	Arg	Arg	Ser		840
	TTC Phe 240	GAG Glu	GC G1	y A	GGC Arg	ATC Ile	TGT Cys 245	GCC Ala	TGT Cys	CCT Pro	GGC Gly	CGT Arg 250	GAC Asp	Arg CGC	AAA Lys	GCT Ala	GAT Asp 255		888
	GAA Glu	GAC Asp	CA Hi	T 1	ryr	CGG Arg 260	GAG Glu	CAA Gln	CAG Gln	GCT Ala	CTG Leu 265	AAT Asn	GAA Glu	AGT Ser	ACC	ACC Thr 270	AAA Lys		936
2	TAA neA	GGA Gly	GC Al	a	CC Lla 175	AGC Ser	AAA Lys	CGT Arg	GCA Ala	TTC Phe 280	AAG Lys	CAG Gln	AGC Ser	CCC Pro	CCT Pro 285	GCC Ala	ATC Ile	•	984
Į	Pro	GCC Ala	CT Le 29	u	GT ly	ACC Thr	AAC Asn	GTG Val	AAG Lys 295	AAG Lys	AGA Arg	CGC Arg	CAC His	GGG Gly 300	GAC Asp	GAG Glu	GAC Asp		1032
P	ATG (et	TTC Phe 305	TA Ty	C A	IG (CAC His	GTG Val	CGA Arg 310	GGC Gly	CGG Arg	GAG Glu	AAC Asn	TTT Phe 315	GAG Glu	ATC Ile	TTG Leu	ATG Met		1080
-	AA .ys .20	GTC Val	AA Ly	G G S G	AG 1	ser	CTA Leu 325	GAA Glu	CTG Leu	ATG Met	GAG Glu	CTT L u 330	GTG Val	CCC Pro	CAG Gln	CCT Pro	TTG Leu 335	`	1128
V	TT al	GAC Asp	TC:	T.	Ar b	CGA Arg 340	CAG Gln	CAG Gln	CAG Gln	CAG Gln	CAG Gln 345	CAG Gln	CTC Leu	CTA Leu	CAG Gln	AGG Arg 350	CCG Pro		1176
A	.GT	CAC	CT	3 C	AG (CT	CCA,	TCC 1	TAT	GGG	ccc	GTG (CTC	TCC	CCA	ATG	AAC		1224

	Sei	His	E Lei	u Glr 355	Pro	Pro	Ser	Tyr	Gly 360	Pro	Val	. Leu	ı Ser	Pro -365		Asn			
	AAC Lys	GTA Val	A CAG His 370	s Gly	GGT Gly	GTC Val	AAC L Asn	AAA Lys 375	Leu	CCC Pro	TCC Ser	GTC Val	AAC Asn 380	Gln	CTG	GTG Val		1272	
	- GGC Gly	G1: 385	/ Pro	CCC Pro	CCG Pro	CAC His	AGC Ser 390	Ser	GCA Ala	GCT Ala	GGG Gly	Pro 395	Asn	CTG Leu	GGG Gly	CCC		1320	
	ATG Met 400	Gly	: TC	GGG Gly	ATG Met	CTC Leu 405	AAC Asn	AGC Ser	CAC His	GGC Gly	CAC His 410	Ser	ATG Met	CCG Pro	GCC Ala	AAT Asn 415		1368	
	GIĄ	Glu	Met	: Asn	G1 y	Gly	CAC His	Ser	Ser	Gln 425	Thr	Met	Val	Ser	Gly 430	Ser		1416	
	CAC	TGC Cys	ACC Thr	CCG Pro 435	CCA Pro	Pro	Pro	TAT Tyr	CAT His 440	GCA Ala	GAC Asp	CCC Pro	AGC Ser	CTC Leu 445	GTC Val	AGT Ser		1464	
	TTT	TTG Leu	ACA Thr 450	Gly	TTG Leu	GG ò Gly	TGT	CCA Pro 455	AAC Asn	TGC Cys	ATC Ile	GAG Glu	TGC Cys 460	TTC Phe	ACT Thr	TCC Ser		1512	
	CAA Gln	GGG Gly 465	TTG Leu	CAG Gln	AGC Ser	Ile	TAC Tyr 470	Nis	CTG Leu	CAG Gln	AAC Asn	CTT Leu 475	ACC Thr	ATC Ile	GAG Glu	GAC Asp		1560	
	CTT Leu 480	GGG Gly	GCT Ala	CTG Leu	AAG Lys	GTC Val 485	Pro	GAC Asp	CAG Gin	TAC Tyr	CGT Arg 490	ATG Met	ACC Thr	ATC Ile	TGG Trp	AGG Arg 495		1608	
	GGC Gly	CTA Leu	CAG Gln	GAC Asp	CTG Leu 500	AAG Lys	CAG Gln	AGC Ser	CAT His	ASP 505	TGC Cys	GGC Gly	CAG Gln	CAA Gln	CTG Leu 510	CTA Leu		1656	١.
	Arg	TCC Ser	AGC Ser	AGC Ser 515	AAC Asn	GCG Ala	GCC Ala	ACC Thr	ATC Ile 520	TCC Ser	ATC Ile	GGC	GGC Gly	TCT Ser 525	GGC Gly	GAG Glu		1704	
-	CTG Leu	CAG Gln	CGG Arg 530	CAG Gln	CGG Arg	GTC Val	ATG Met	GAA Glu 535	GCC Ala	GTG Val	CAT His	TTC Phe	CGT Arg 540	GTG Val	CGC	CAC His		1752	
	ACC Thr	ATC Ile 545	ACA Thr	ATC Ile	CCC Pro	AAC Asn	CGT Arg 550	GGA Gly	G1 y	GCA Ala	Gly	GCG Ala 555	GTG Val	ACA Thr	GGT [*] Gly	CCC Pro		1900	
	GAC Asp 560	GAG Glu	TGG Trp	GCG Ala	GAC Asp	TTT Phe 565	GGC Gly	TTT Phe	GAC Asp	CTG Leu	CCT Pro 570	GAC Asp	TGC Cys	AAG Lys	Se ' t	CGT Arg 575		1848	
	AAG Lys	CAG Gln	CCC Pro	Ile	AAA Lys 580	GAG Glu	GAG Glu	TTC . Phe	Thr	GAG Glu 585	ACA Thr	GAG Glu	AGC Ser	CAC His				1890	
	TGAG	GAAC	GT A	CCTT	CTTC	тсс	TGTC	CTTC	CTC	TGTG.	AGA	AACT	GCTC	TT G	gaag	TGGGA		1950	
	CCTG	TTGG	CT G	TGCC	CACA	g aa	ACCA	GCAA	GGA	CCTT	CTG	cccc	ATGC	CA T	TCCT	GAAGG	. \	2010	
•	GAAG'	ICGC	TC A	TGAA	CTAA	с тс	CCTC	TTGG									;	2040	

(2) INFORMATION FOR SEQ ID NO: 8:

⁽i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 589 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Cys Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe Asn $\frac{1}{2}$ 15

Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro Ala 20 25 30

Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser Pro
40
45

Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val
50 60

Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr 65 70 75 80

Phe Gln Gln Ser Set Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro

Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln
100 105 110

Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met

Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys Arg Cys 130

Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro 150 155 160

Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ala Gln Tyr Val 165 175

Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro 180 185

Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Deu Tyr Asn Phe Met Cys 195 200

Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Aro Ile Leu Val Ile 210 215

Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe 225 235 240

Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu 245 255

Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Thr Thr Lys Asn 260 265

Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Ile Pro 275 280 285

Ala Leu Gly Thr Asn Val Lys Lys Arg Arg His Gly Asp Glu Asp Met 290 295 300

Phe Tyr Met His Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys 305 310 315

Val Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val 325 330 335

Asp Ser Tyr Arg Gln Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser 340 345 350

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys

m

(ii) MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 8: Met Cys\Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro Ala Ser Pro Tyr thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser Pro
40
45 Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn The Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln Gln Ser Ser The Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln 100 105 110 Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys Arg Cys Pro Asn His Glu Leu Gly Arg Asp Pha Asn Glu Gly Gln Ser Ala Pro 145 150 160 Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ala Gln Tyr Val 165 170 175 Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro 180 185 190 Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys 195 200 Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro le Leu Val Ile 210 220 Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu 255 Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Thr Thr Lys Asn 260 265 270 Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Ile Pro 275 280 285 Ala Leu Gly Thr Asn Val Lys Lys Arg Arg His Gly Asp Glu Asp Met 290 295 300 Phe Tyr Met His Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Val Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu S r Pro Met Asn Lys

. '	Val	. Hi:	s -G1)	y Gl	y Val	l Asr	1 Lys 375	Leu	Pro	Ser	va:	L Asn 380	Glr	ı Leu	ı Val	. Gly
	51r 385	Pro	o Pr	o Pro	o His	3 Ser 390	Ser	Ala	Ala	Gly	/ Pro	Asn		. Gly	Pro	Met 400
(31 y	Sez	G1	y Met	Leu 405	ı Asn	Ser	His	Gly	His 410	Ser	Met	Pro	Ala	Asn 415	
(Glu	Met	: Asi	n G1 y	/ .Gly	/ His	Ser	Ser	Gln 425	Thr	Met	Val	Ser	Gly 430	Ser	His
(:ys	Thr	Pro 439	2 P z d	Pro	Pro	Tyr	His 440	Ala	Asp	Pro	Ser	Leu 445	Val	Ser	Phe
I	eu	Thr 450	Gly	y Leu	GIY	Суз	Pro 455	Asn	Суз	Ile	Glu	Cys 460	Phe	Thr	Ser	Gln
4	1 y 65	Leu	Glr	n Ser	Ile	T) r 478	His	Leu	Gln	Asn	Leu 475	Thr	Ile	Glu	Asp	Leu 480
G	ly	Ala	Leu	Lys	Val 485	Pro	Asp	Gln	Tyr	Arg 490	Met	Thr	Île	Trp	Arg 495	Gly
L	eu	Gln	Asp	500	Lys	Gln	Ser	His	Asp 505	СЛè	Gly	Gln	Gln	Leu 510	Leu	Arg
s	er	Ser	Ser 515	Asn	Ala	Ala	Thr	11e 520	Ser	Ile	Gly	Gly	Ser 525	Gly	Gĺu	Leu
G	ln	Arg 530	Gln	Arg	Val	Met	Glu 535	Ala	val	His	Phe	Arg 540	Val	Arg	His	Thr
5	1e 45	Thr	Ile	Pro	Asn	Arg 550	Gly	Gly	Ala	cz/A	Ala 555	Val	Thr	Gly	Pro	Asp 560
G.	lu	Trp	Ala	qzA	Phe 565	Gly	Phe	qeA	Leu	Pro 570	Asp.	Суз	Lys	Ser	Arg 575	Lys
G:	ln	Pro	Ile	Lys 580	Glu	Glu	Phe	Thr	Glu 585	Thr	Glu	Ger	His			

- (2) INFORMATION FOR SEQ ID NO: 9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 758 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (Vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mus musculus
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 389..757
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGGTCCCGCT TCGACCAAGA CTCCGGCTAC CAGCTTGCGG GCCCCGCGGA GGAGGAGACC CCGCTGGGGC TAGCTGGGCG ACGCGCGCCA AGCGGCGGCG GGAAGGAGGC GGGAGGAGCG GGGCCCGAGA CCCCGACTCG GGCAGAGCCA GCTGGGGAGG CGGGGCGCGC GTGGGAGCCA GGGGCCCGGG TGGCCGGCCC TCCTCCGCCA CGGCTGAGTG CCCGCGCTGC CTTCCCGCCG

120

130

GTC	CGCC	AAG	AAAG	GCGC	TA A	GCCT	GCGG	C AG	TCCC	CTCG	CCG	CCGC	CTC	CCTG	CTCC	GC 300
ACC	CTTA	TAA	CCCG	CCGT	cc c	GCAT	CCAG	G CG	AGGA	GGCA	ACG	CTGC	AGC	CCAG	CCCT	G 360
cce	ACGC	CGA	cccc	CGGC	cc G	GAGC	AĢA	ATG Met	AGC Ser	GGC Gly	AGC Ser	GTT Val 5	GGG Gly	GAG Glu	ATG Met	412
GCC Ala	CAG Gln 10	\Thr	TCT Ser	TCT Ser	TCC Ser	TCC Ser 15	TCC Ser	TCC Ser	ACC Thr	TTC Phe	GAG Glu 20	His	CTG Leu	TGG Trp	AGT Ser	. 460
TCT Ser 25	Leu	GAG Glu	CCA Pro	GAC Asp	AGC Ser 30	ACC Thr	TAC Tyr	TTT Phe	GAC Asp	CTC Leu 35	CCC Pro	CAG Gln	Pro	AGC Ser	CAA Gln 40	508
GGG Gly	ACT	AGC Ser	GAG Glu	GCA Ala 45	TCA Ser	Gly	AGC Ser	GAG Glu	GAG Glu 50	TCC Ser	AAC Asn	ATG Met	GAT Asp	GTC Val 55	TTC Phe	556
CAC His	CTG Leu	CAA Gln	GGC Gly 60	ATG Met	GCC Ala	CAG Gln	TTC Phe	AAT Asn 65	TTG Leu	CTC Leu	AGC Ser	AGT Ser	GCC Ala 70	ATG Met	GAC Asp	604
CAG Gln	ATG Met	GGC Gly 75	AGC Ser	CGT Arg	GCG Ala	CC Ala	CCG Pro 80	GCG Ala	AGC Ser	CCC	TAC Tyr	ACC Thr 85	CCG Pro	G AG Glu	CAC	652
GCC Ala	GCC Ala 90	AGC Ser	GCG Ala	CCC Pro	ACC Thr	CAC His 95	ACG Ser	CCC Pro	TAC Tyr	GCG Ala	CAG Gln 100	CCC	AGC Ser	TCC Ser	ACC Thr	700
TTC Phe 105	GAC Asp	ACC Thr	ATG Met	TCT Ser	CCG Pro 110	GCG Ala	CCT Pro	Aar Garc	ATC Ile	CCT Pro 115	TCC Ser	ÀAT Asn	ACC Thr	GAC Asp	TAC Tyr 120	, 748
	GGC Gly		С	•									•			7.58

INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ser Gly Ser Val Gly Glu Met Ala Gln Thr Ser Ser Ser Ser 1 5 10

Ser Thr Phe Glu His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr 20 25 30

Phe Asp Leu Pro Gln Pro Ser Gln Gly Thr Ser Glu Ala Ser Gly Ser

Glu Glu Ser Asn Met Asp Val Phe His Leu Gln Gly Met Ala Gln Phe 50 60

Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro 65 70 75 90

Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser 85 90 95

Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro 115 120 (2) INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: (A) LENGTH: 559 base pairs (3) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (vi) ORIGINAL SOURCE: QRGANISM: Homo sapiens (A) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11: CGACCTTCCC CAGTCAAGCC GGGGGAATAA TGAGGTGGTG GGCGGAACGG ATTCCAGCAT 60 GGACGTCTTC CACCTGGAGG GCATGACTAC ATCTGTCATG CATCCTCGGC TCCTGCCTCA 120 CTAGCTGCGG AGCCTCTCCC CCTCGGTCCA CGCTGCCGGG CGGCCACGAC CGTGACCCTT 180 CCCCTCGGGC CGCCCAGATC CATGCCTCGT CCCACGGGAC ACCAGTTCCC TGGCGTGTGC 240 AGACCCCCCG GCGCCTACCA TGCTGTACGT CGGTGACCCC GCACGGCACC TCGCCACGGC 300 CCAGTTCAAT CTGCTGAGCA GCACCATGGA CCAGATGAGC AGCCGCGGG CCTCGGCCAG 360 CCCCTACACC CCAGAGCACG CCGCCAGCGAG GCCCACCCAC TCGCCCTACG CACAACCCAG 420 CTCCACCTTC GACACCATGT CGCCGGCGCC TGTCATCCCC TCCAACACCG ACTACCCCGG 480 ACCCCACCAC TITGAGGICA CITTCCAGCA GICCAGCACG GCCAAGTCAG CCACCIGGAC 540 GTACTCCCCG CTCTTGAAG 559 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: (A) LENGTH: 1764 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12: ATGCTGTACG TCGGTGACCC CGCACGGCAC CTCGCCACGG CCCAGTTCAA TCTGTGAGC 60 AGCACCATGG ACCAGATGAG CAGCCGCGCG GCCTCGGCCA GCCCCTACAC CCCAGAGCAC 120 GCCGCCAGCG TGCCCACCCA CTCGCCCTAC GCACAACCCA GCTCCACCTT CGACACCATG 180 TOGOCOGOGO CTGTCATCCC CTCCAACACC GACTACCCCG GACCCCACCA CTTTGAGGTC 240 ACTITCCAGO AGTOCAGOAC GGCCAAGTCA GCCACCTGGA CGTACTCCCC GCTCTTGAAG

AAACTCTACT GCCAGATCGC CAAGACATGC CCCATCCAGA TCAAGGTGTC CACCCCGCCA

CCCCCAGGCA CTGCCATCCG GGCCATGCCT GTTTACAAGA AAGCGGAGCA CGTGACCGAC

GTCGTGAAAC GCTGCCCCAA CCACGAGCTC GGGAGGGACT TCAACGAAGG ACAGTCTGCT

300

3/60

420

CCAGCCAGCC ACCTCATCCG CGTGGAAGGC AATAATCTCT CGCAGTATGT GGATGACCCT 540 GTCACCGGCA GGCAGAGCGT CGTGGTGCCC TATGAGCCAC CACAGGTGGG GACGGAATTC 600 ACCACCATCC TGTACAACTT CATGTGTAAC AGCAGCTGTG TAGGGGGCAT GAACCGGCGG 660 COCATOCTEA TOATCATOAC COTGGAGATG CGGGATGGGC AGGTGCTGGG CCGCCGGTCC 720 CCATCTGCGC CTGTCCTGGC CGCGACCGAA AAGCTGATGA GGACCACTAC TTTGAGGGCC 780 CGGGAGCAGC AGGCCCTGAA CGAGAGCTCC GCCAAGAACG GGGCCGCCAG CAAGCGTGCC 940 TTCAAGCAGA GCCCQCCTGC CGTCCCCGCC CTTGGTGCCG GTGTGAAGAA GCGGCGGCAT 900 GGAGACGAGG ACACGTÀCTA CCTTCAGGTG CGAGGCCGGG AGAACTTTGA GATCCTGATG 96Ò AAGCTGAAAG AGAGCCTGÒA GCTGATGGAG TTGGTGCCGC AGCCACTGGT GGACTCCTAT 1020 CGGCAGCAGC AGCAGCTCCT ACAGAGGCCG AGTCACCTAC AGCCCCCGTC CTACGGGCCG 1080 GTCCTCTCGC CCATGAACAA GOTGCACGGG GGCATGAACA AGCTGCCCTC CGTCAACCAG 1140 CTGGTGGGCC AGCCTCCCCC GCACAGTTCG GCAGCTACAC CCAACCTGGG GCCCGTGGGC 1200 CCCGGGATGC TCAACAACCA TGGCCAGGCA GTGCCAGCCA ACGGCGAGAT GAGCAGCAGC 1260 CACAGGGCC AGTCCATGGT CTCGGGGTTC CACTGCACTC CGCCACCCC CTACCACGCC 1320 GACCCCAGCC TCGTCAGTTT TTTAACAGGA TTGGGGTGTC CAAACTGCAT CGAGTATTTC 1380 ACCTCCCAAG GGTTACAGAG CATTTACCAC CTGCAGAACC TGACCATTGA GGACCTGGGG 1440 GCCCTGAAGA TCCCCGAGCA GTACCGCATG ACCARCTGGC GGGGCCTGCA GGACCTGAAG 1500 CAGGGCCACG ACTACAGCAC CGCGCAGCAG CTGCTCCGCT CTAGCAACGC GGCCACCATC 1560 TCCATCGGCG GCTCAGGGGA ACTGCAGCGC CAGCGGGTC% TGGAGGCCGT GCACTTCCGC 1620 GTGCGCCACA CCATCACCAT CCCCAACCGC GGCGGCCCAG GCGGCGGCCC TGACGAGTGG 1680 GCGGACTTCG GCTTCGACCT GCCCGACTGC AAGGCCCGCA AGQAGCCCAT CAAGGAGGAG 1740 TTCACGGAGG CCGAGATCCA CTGA 1764

INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:.

Met Leu Tyr Val Gly Asp Pro Ala Arg His Leu Ala Thr Ala Gln Ahe

Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala Ser

Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His Ser

Pro Tyr Ala Gin Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val

(3

Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile 31A lle Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr 165 170 Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met 195 200 Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile 210 220 Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg Ser 225 230 240 Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp 245 250 250 Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys Arg Ala the Lys Gln Ser Pro Pro Ala Val 275 280 285 Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp 290 295 Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met 305 310 320 Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Let Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gan Arg Pro Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Wal Gly Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His dys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Leu 440 Thr Gly Leu Gly Cys Pro Asn Cys Il Glu Tyr Phe Thr Ser Gln Gly

Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly 470 Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu 485 490 Gan Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu 510 Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Arg Ser Gln Arg GMn Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr 530 Ile Thr Ile Pao Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp 545 550 Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu Glu Phe Nor Glu Ala Glu Ile His 580

(2) INFORMATION FOR SEQ ID NO 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

TCGGTGACCC CGCACGGCAC CTCGCCACGG CCQAGTTCAA TCTGCTGAGC 60 AGCACCATGG ACCAGATGAG CAGCCGCGCG GCCTCGGCCA GCCCCTACAC CCCAGAGCAC 120 GCCGCCAGCG TGCCCACCCA CTCGCCCTAC GCACAACCCA GCTCCACCTT CGACACCATG 130 TCGCCGGCGC CTGTCATCCC CTCCAACACC GACTACCCCG GACCCCACC CTTTGAGGTC 240 ACTITICAGE AGTICAGEAC GGCCAAGTEA GCCACCTGGA CGTACTCCCC OCTICTTGAAG 300 AAACTCTACT GCCAGATCGC CAAGACATGC CCCATCCAGA TCAAGGTGTC CACCCGCCA 360 CCCCCAGGCA CTGCCATCCG GGCCATGCCT GTTTACAAGA AAGCGGAGCA CGTGAGCGAC 420 GTCGTGAAAC GCTGCCCCAA CCACGAGCTC GGGAGGGACT TCAACGAAGG ACAGTCTOCT 480 CCAGCCAGCC ACCTCATCCG CGTGGAAGGC AATAATCTCT CGCAGTATGT GGATGACCCT 540 GTCACCGGCA GGCAGAGCGT CGTGGTGCCC TATGAGCCAC CACAGGTGGG GACGGAATTC 600 ACCACCATCC TGTACAACTT CATGTGTAAC AGCAGCTGTG TAGGGGGGCAT GAACCGGCGG 660 CCCATCCTCA TCATCATCAC CCTGGAGATG CGGGATGGGC AGGTGCTGGG CCGCCGGTCC 720 TTTGAGGGCC GCATCTGCGC CTGTCCTGGC CGCGACCGAA AAGCTGATGA GGACCACTAC 780 CGGGAGCAGC AGGCCCTGAA CGAGAGCTCC GCCAAGAACG GGGCCGCCAG CAAGCGTGCC 940 TTCAAGCAGA GCCCCCCTGC CGTCCCCGCC CTTGGTGCCG GTGTGAAGAA GCGGCGGCAT 900 GGAGACGAGG ACACGTACTA CCTTCAGGTG CGAGGCCGGG AGAACTTTGA GATCCTGATG 960

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AAGCTGAAAG	AGAGCCTGGA	GCTGATGGAG	TTGGTGCCGC	AGCCACTGGT	GGACTCCTAT	102
CGGCAGCAGC	AGCAGCTCCT	ACAGAGGCCG	CCCCGGGATG	CTCAACAACC	ATGGCCACGC	108
AGTÓCCAGCC	AACGGCGAGA	TGAGCAGCAG	CCACAGCGCC	CAGTCCATGG	TCTCGGGGTC	114
ссастосаст	CCGCCACCCC	CCTACCACGC	CGACCCCAGC	CTCGTCAGGA	CCTGGGGGCC	1200
CIGAAGAICC	CCGAGCAGTA	CCGCATGACC	ATCTGGCGGG	GCCTGCAGGA	CCTGAAGCAG	1260
GGCCACGACT	ACAGCACCGC	GCAGCAGCTG	CTCCGCTCTA	GCAACGCGGC	CACCATCTCC	1320
ATCGGCGGCT	CAGGGGAACT	GCAGCGCCAG	CGGGTCATGG	AGGCCGTGCA	CTTCCGCGTG	1380
CGCCACACCA	TCACCATCCC	CAACCGCGGC	GGCCCAGGCG	GCGGCCCTGA	CGAGTGGGCG	1440
GACTTCGGCT	TCGACQTGCC	CGACTGCAAG	GCCCGCAAGC	AGCCCATCAA	GGAGGAGTTC	1500
ACGGÄGGCCG	AGATCCACTG	A				1521

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 amino acids
 (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Met Leu Tyr Val Gly Asp Pro Ala Arg His Leu Ala Thr Ala Gln Phe

Asn Leu Leu Ser Ser Thr Met Asp Gin Met Ser Ser Arg Ala Ala Ser

Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His Ser

Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro 50 55

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro Xis His Phe Glu Val 65 70 75

Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser

Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Tha Cys Pro Ile 100

Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala

Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Arg 135

Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala 150

Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr

Val Asp Asp Pro Val Thr Gly Arg Gln S r Val Val Val Pro Tyr Glu
180 185 190

Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met

Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asa His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu Aly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gla Gln Gln Leu Leu Gln Arg Pro Pro Arg 340 Asp Ala Gln Gln Pro Trp Pao Arg Ser Ala Ser Gln Arg Arg Asp Glu Gln Gln Pro Gln Arg Pro Val Ais Gly Leu Gly Val Pro Leu His Ser Ala Thr Pro Leu Pro Arg Arg Pro Gln Pro Arg Gln Asp Leu Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln 405 Asp Leu Lys Gln Gly His Asp Tyr Ser The Ala Gln Gln Leu Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln
435 Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp Ala 465 470 475 480 Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1870 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 104..1867

	. ,	(xi) SI	EQUEN	ICE E	ESCF	IPTI	ON:	SEQ	ID N	10: 1	6:						
	TGC	ccg	GGC	TGC	AÇGO	cr c	CAGO	GAAC	C AG	ACAG	CACC	TAC	TTCG	ACC	TTCC	CCAG	TC	60
	AAG	ccsc	egéc	AATA	ATGA	GG I	GGTG	GGCG	G AA	.CGGA	TTCC	AGC				TTC Phe	•	115
	CAC His	Let	GAC Glu	r Gra	ATC	ACT Thr 10	Thr	TCT Ser	GTC Val	ATG Met	GCC Ala 15	CAG Gln	TTC Phe	AAT Asn	CTG Leu	CTG Leu 20		163
	AGC Ser	AGC	ACC Thr	ATG Met	GAC Asp 25	CAG Gln	ATG Met	AGC Ser	AGC Ser	CGC Arg 30	GCG Ala	GCC Ala	TCG Ser	GCC Ala	AGC Ser 35	Pro		211
	Tyr	Thr	Pro	61u 40	. His	Alla	Ala \	Ser	Val 45	Pro	Thr	His	Ser	Pro 50	Tyr	GCA Ala		259
	Gln	Pro	Ser 55		Thr	Phe	ASID	Thr 60	Met	Ser	Pro	Ala	Pro 65	Val	Ile	Pro		307
	Ser	Asn 70	Thr	dsV.	Tyr	Pro	Gly 75	Pi	His	His	Phe	Glu 80	Val	Thr	Phe	CAG Gln		355
	Gln 85	Ser	Ser	Thr	Ala	Lys 90	Ser	Ala	THE	Trp	Thr 95	Tyr	Ser	Pro	Leu	100		403
	AAG Lys	AAA Lys	Leu	TAC Tyr	TGC Cys 105	CAG Gln	ATC Ile	GCC Ala	AAG Lys	ACA The 110	TGC Cys	CCC	ATC Ile	CAG Gln	ATC Ile 115	AAG Lys		451
	GTG Val	TCC Ser	ACC Thr	CCG Pro 120	CCA Pro	CCC Pro	CCA Pro	GGC Gly	ACT Thr 125	GCC Ala	ATC Ile	CGG Arg	GCC Ala	ATG Met 130	CCT	GTT Val		499
(TAC Tyr	AAG Lys	AAA Lys 135	GCG Ala	GAG Glu	CAC His	GTG Val	ACC Thr 140	GAC Asp	GTC Val	GTG Val	AAA Lys	CGC Arg 145	TGC Cys	CCC Pro	AAC Asn		547
'	CAC His	GAG Glu 150	CTC Leu	GGG Gly	AGG Arg	GAC Asp	TTC Phe 155	AAC Asn	GAA Glu	GGA Gly	CAG Gln	TCT Ser 160	AL A	CCA Pro	GCC Ala	AGC Ser		595
	CAC His 165	CTC Leu	ATC Ile	CGC Arg	GTG Val	GAA Glu 170	GGC	AAT Asn	AAT Asn	CTC Leu	TCG Ser 175	CAG Gln	TAT Tyr	GTG Val	GAT Asp	GAC Asp 180		643
	CCT Pro	GTC Val	ACC Thr	GGC Gly	AGG Arg 185	CAG Gln	AGC Ser	GTC Val	GTG Val	GTG Val 190	CCC Pro	TAT Tyr	GAG Glu	CCA Pro	CCA Pro 195	CAG Gln		691
	GTG Val	GGG Gly	ACG Thr	GAA Glu 200	TTC Phe	ACC	ACC Thr	ATC Ile	CTG Leu 205	TAC Tyr	AAC Asn	TTC Phe	ATG Met	TGT Cys 210	AAC Asn	AGC Sez	\	739
	AGC Ser	TG T Cys	GTA Val 215	GGG Gly	GGC Gly	ATG Met	AAC Asn	CGG Arg 220	CGG Arg	CCC Pro	ATC Il	CTC Leu	ATC Ile 225	ATC Ile	ATC Ile	ACC Thr		787
	CTG Leu	GAG Glu 230	ATG Met	CGG Arg	GAT Asp	GGG Gly	CAG Gln 235	GTG Val	CTG Leu	GGC Gly	CGC Arg	CGG Arg 240	TCC	TTT Phe	GAG Glu	GGC Gly	`	835
	CGC	ATC	TGC	GCC	TGT	CCT	GGC	CGC	GAC	CGA	AAA	GCT	GAT	GAG	GAC	CAC		883

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(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 amino acids
 - (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala 20 30

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His

Ser Pro Tyr Ala Gln Pro Ser Ser Thr the Asp Thr Met Ser Pro Ala
50 55

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu 65 70 80

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
85 90 95

Ser Pro Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg 115

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
130 135 140

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln 165

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Pro Tyr

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Led 210 220

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg 235 240

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Clu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala\Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu 290 295 300 Asp Thr Tyr Tyx Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys 355 360 365 Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly 370 380 Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met Leu Asn Asn His\Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser His Ser Ala Glo Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln Leu Gln Ser Ile Tyr His Leu Gln Asn Lau Thr Ile Glu Asp Leu 470 473 Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu 500 505 Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Pro Asp Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1817 base pairs

Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MQLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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	ATGGCCCAGT	CCACCGCRAC	CTCCCCTGÀT	GGGGGCACCA	CGTTTGAGC	CCTCTGGAGC	60
	TCTCTGGAAC	CAGACAGCA	CTACTTCGAC	CTTCCCCAGI	CAAGCCGGG	GAATAATGAG	120
-	GTGGTGGGCG	GAACGGATTC	CAGCATGGAC	GTCTTCCACC	TGGAGGGCAT	GACTACATCT	180
	GTCATGGCCC	AGTTCAATCT	GTGAGCAGC	ACCATGGACC	AGATGAGCAG	ccecececc	240
	TCGGCCAGCC	CCTACACCCC	AGAGCACGCC	GCCAGCGTGC	CCACCCACTO	GCCCTACGCA	300
	CAACCCAGCT	CCACCTTCGA	CACCATGTCG	CCGGCGCCTG	TCATCCCCT	CAACACCGAC	360 ·
	TACCCCGGAC	CCCACCACTT	TGAGGTGACT	TTCCAGCAGT	CCAGCACGG	CAAGTCAGCC	420
	ACCTGGACGT	ACTCCCCGCT	CTTGAAGAA	CTCTACTGCC	AGATCGCCAA	GACATGCCCC	480
	ATCCAGATCA	AGGTGTCCAC	ccccccaccd	CCAGGCACTG	CCATCCGGG	CATGCCTGTT	540
	TACAAGAAAG	CGGAGCACGT	GACCGACGTC	GIGAAACGCI	GCCCCAACCA	CGAGCTCGGG	600
	ĄGGGACTTCA	ACGAAGGACA	GTCTGCTCCA	GCRAGCCACC	TCATCCGCGT	GGAAGGCAAT	660
	AATCTCTCGC	agtatgtgga	TGACCCTGTC	ACCOGCAGGC	AGAGCGTCGT	GGTGCCCTAT	720
	GAGCCACCAC	AGGTGGGGAC	GGAATTCACC	ACCATOCTGT	ACAACTTCAT	GTGTAACAGC	780
	AGCTGTGTAG	GGGGCATGAA	CCGGCGGCCC	ATCCTCATCA	TCATCACCCT	-GGAGATGCGG	840
	GATGGGCAGG	TGCTGGGCCG	CCGGTCCTTT	GAGGGCCGCA	TCTGCGCCTG	TCCTGGCCGC	900
	GACCGAAAAG	CTGATGAGGA	CCACTACCGG	GAGCAGCAGG	CCCTGAACGA	GAGCTCCGCC	960
/	AAGAACGGGG	CCGCCAGCAA	GCGTGCCTTC	AAGCAGAGCC	cdccreccer	CCCCGCCCTT	1020
	GGTGCCGGTG	TGAAGAAGCG	GCGGCATGGA	GACGAGGACA	CGTACTACCT	TCAGGTGCGA	1080
	GGCCGGGAGA	ACTTTGAGAT	CCTGATGAAG	CTGAAAGAGA	GCCTGGAGCT	GATGGAGTTG	1140
	GTGCCGCAGC	CACTGGTGGA	CTCCTATCGG	CAGCAGCAGC	AGCTCCTACA	GAGGCCGAGT	1200
	CACCTACAGC	CCCGTCCTA	CGGGCCGGTC	CTCTCGCCCA	TGAACAAGOT	GCACGGGGGC	1260
	ATGAACAAGC	IGCCCTCCGT	CAACCAGCTG	GTGGGCCAGC	CTCCCCGCA	CAGTTCGGCA	1320
	GCTACACCCA 2	ACCTGGGGCC	CGTGGGCCCC	GGGATGCTCA	ACAACCATGG	COACGCAGTG	1,380
	CCAGCCAACG	GCGAGATGAG	CAGCAGCCAC	AGCGCCCAGT	CCATGGTCTC	GGGTCCCAC	1440
	TGCACTCCGC (ACCCCCCTA	CCACGCCGAC	CCCAGCCTCG	TCAGGACCTG	GGGGCTGA	1500
	AGATCCCCGA (CAGTACCGC .	ATGACCATCT	GGCGGGGCCT	GCAGGACCTG	AAGCAGGGCC	1560
	ACGACTACAG (ACCGEGCAG	CAGCTGCTCC	GCTCTAGCAA	CGCGGCCACC	ATCTCCATC	1620
	GCGGCTCAGG (GAACTGCAG	CGCCAGCGGG	TCATGGAGGC	CGTGCACTTC	cecerecece	1680
	ACACCATCAC C	ATCCCCAAC	CGCGGCGGCC	CAGGCGGCGG	CCCTGACGAG	TGGGCGGACT	1740
	TCGGCTTCGA C	CTGCCCGAC	IGCAAGGCCC	GCAAGCAGCC	CATCAAGGAG	GAGTTCACGG	1800
	AGGCCGAGAT C	CACTGA	•				1817

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 amino acids
 - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (11) MQLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Ala Gla Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro

Gln Ser Ser Arg\Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln 50

Phe Asn Leu Leu Ser ger Thr Met Asp Gln Met Ser Ser Arg Ala Ala

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr

Ser Pro Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Led Tyr Asn Phe

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lya Ala

Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala

Lys asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala 335
Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu 340
Asp Thr Tyk Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu 355
Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro 370
Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser 385
His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys 415
Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly 425
Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val 435
Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly 450
Glu Met Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His 465
Cys Thr Pro Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr 485
Trp Gly Pro

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCGAGCTGCC CTCGGAG

- (2) INFORMATION FOR SEQ ID NO: 21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (iii) ANTI-SENSE: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

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GGTTCTGGAG GTGACTCAG (2) INFORMATION FOR SEQ ID NO: 22: (i) SEQUENCE CHARACTERISTICS: LENGTH: 18 base pairs (B) XYPE: nucleic acid STRANDEDNESS: single (D) TOROLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22: GCCATGCCTG TCTACAAG (2) INFORMATION FOR SEQ ID NO: 23: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 23: ACCAGCTGGT TGACGGAG (2) INFORMATION FOR SEQ ID NO: 24: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24: GTCAACCAGC TGGTGGGCCA G (2) INFORMATION FOR SEQ ID NO: 25: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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STRANDEDNESS: single
                TOPOLOGY: linear
      (ii) MOLECULE TYPE: DNA
     (iii) ANTI-SANSE: NO
     (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 AGGCCGGCGT GGGGAAG
 (2) INFORMATION FOR SEQ ID NO: 27:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 19 pase pairs
           (B) TYPE: nucleit acid
(C) STRANDEDNESS: single
           (D) TOPOLOGY: lineer
     (ii) MOLECULE TYPE: DNA
    (iii) ANTI-SENSE: YES
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
CTTGGCGATC TGGCAGTAG
(2) INFORMATION FOR SEQ ID NO: 28:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 17 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA
   (iii) ANTI-SENSE: NO
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:
GCGGCCACGA CCGTGAC
(2) INFORMATION FOR SEQ ID NO: 29:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA
   (iii) ANTI-SENSE: YES
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GTGGATCTCG GCCTCC

(2) INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid

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GGCAGCTTGG GTCTCTGG (2) INFORMATION FOR SEQ ID NO: 30: (i) SEQUENCE CHARACTERISTICS: (A) LINGTH: 18 base pairs (B) TYRE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYRE: DNA (iii) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30: CTGTACGTCG GTGACCCC (2) INFORMATION FOR SEQ ID NO: 31: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base paixs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31: TCAGTGGATC TCGGCCTC INFORMATION FOR SEQ ID NO: 32: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32: AGGGGACGCA GCGAAACC (2) INFORMATION FOR SEQ ID NO: 33: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

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CCATÇAGCTC CAGGCTCTC (2) INTORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (N) TOPOLOGY: linear (11) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34: CCAGGACAGG CGCAGATG (2) INFORMATION FOR SEQ ID NO: 35: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: gingle (D) TOPOLOGY: lineal (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35: GATGAGGTGG CTGGCTGGA (2) INFORMATION FOR SEQ ID NO: 36: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (iii) ANTI-SENSE: YES (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36: TGGTCAGGTT CTGCAGGTG (2) INFORMATION FOR SEQ ID NO: 37: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (i1) MOLECULE TYPE: DNA (111) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

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CACCTACTC AGGGATGC
                                                                                     18 .
 (2) INFORMATION FOR SEQ ID NO: 38:
       (1) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 21 base pairs
             (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: DNA
    (iii) ANTI-SENSE: YES
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
AGGAAAATAG AAGCGTCAGT C
                                                                                  . 21
 (2) INFORMATION FOR SEQ ID NO: 39:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DN
    (iii) ANTI-SENSE: NO
     (xi) SEQUENCE DESCRIPTION:\seq ID NO: 39:
CAGGCCCACT TGCCTGCC
                                                                                    18
(2) INFORMATION FOR SEQ ID NO: 40:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 19 base pair
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA
    (iii) ANTI-SENSE: YES
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
CTGTCCCCAA GCTGATGAG
```